



SEQUENCE LISTING

<110> JOHNSON, BRUCE FLETCHER
SYUD, FAISAL

<120> LABELED PEPTIDES FOR LECTIN-LIKE OXIDIZED LOW-DENSITY
LIPOPROTEIN RECEPTOR (LOX-1)

<130> 61765.002009

<140> 10/691,532

<141> 2003-10-24

<160> 11

<170> PatentIn Ver. 3.2

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<211> 5

<212> PRT

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Synthetic
peptide

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Leu Ser Xaa Pro Pro

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peptide

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Leu Thr Pro Ala Xaa Ala

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5

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ttggaa atg act ttt gat gac cta aag atc cag act gtg aag gac cag      168
    Met Thr Phe Asp Asp Leu Lys Ile Gln Thr Val Lys Asp Gln
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cct gat gag aag tca aat gga aaa aaa gct aaa ggt ctt cag ttt ctt      216
Pro Asp Glu Lys Ser Asn Gly Lys Lys Ala Lys Gly Leu Gln Phe Leu
    15             20             25             30

tac tct cca tgg tgg tgc ctg gct gct gcg act cta ggg gtc ctt tgc      264
Tyr Ser Pro Trp Trp Cys Leu Ala Ala Ala Thr Leu Gly Val Leu Cys
        35             40             45

ctg gga tta gta gtg acc att atg gtg ctg ggc atg caa tta tcc cag      312
Leu Gly Leu Val Val Thr Ile Met Val Leu Gly Met Gln Leu Ser Gln
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gtg tct gac ctc cta aca caa gag caa gca aac cta act cac cag aaa      360
Val Ser Asp Leu Leu Thr Gln Glu Gln Ala Asn Leu Thr His Gln Lys
        65             70             75

aag aaa ctg gag gga cag atc tca gcc cgg caa caa gca gaa gaa gct      408
Lys Lys Leu Glu Gly Gln Ile Ser Ala Arg Gln Gln Ala Glu Glu Ala
    80             85             90

tca cag gag tca gaa aac gaa ctc aag gaa atg ata gaa acc ctt gct      456
Ser Gln Glu Ser Glu Asn Glu Leu Lys Glu Met Ile Glu Thr Leu Ala
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cgg aag ctg aat gag aaa tcc aaa gag caa atg gaa ctt cac cac cag      504
Arg Lys Leu Asn Glu Lys Ser Lys Glu Gln Met Glu Leu His His Gln
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Asn Leu Asn Leu Gln Glu Thr Leu Lys Arg Val Ala Asn Cys Ser Ala
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ttg gat gcc aag ttg ctg aaa att aat agc aca gct gat ctg gac ttc      696
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195 200 205

tct cgg agg aac ccc agc tac cca tgg ctc tgg gag gac ggt tct cct 792
Ser Arg Arg Asn Pro Ser Tyr Pro Trp Leu Trp Glu Asp Gly Ser Pro
210 215 220

ttg atg ccc cac tta ttt aga gtc cga ggc gct gtc tcc cag aca tac 840
Leu Met Pro His Leu Phe Arg Val Arg Gly Ala Val Ser Gln Thr Tyr
225 230 235

cct tca ggt acc tgt gca tat ata caa cga gga gct gtt tat gcg gaa 888
Pro Ser Gly Thr Cys Ala Tyr Ile Gln Arg Gly Ala Val Tyr Ala Glu
240 245 250

aac tgc att tta gct gcc ttc agt ata tgt cag aag aag gca aac cta 936
Asn Cys Ile Leu Ala Ala Phe Ser Ile Cys Gln Lys Lys Ala Asn Leu
255 260 265 270

aga gca cag tgaatttgaa ggctctggaa gaaaagaaaa aagtctttga 985
Arg Ala Gln

gttttattct ggaatttaag ctattctttg tcacttgggt gccaaacatg agagcccaga 1045
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35 40 45
Leu Val Val Thr Ile Met Val Leu Gly Met Gln Leu Ser Gln Val Ser
50 55 60
Asp Leu Leu Thr Gln Glu Gln Ala Asn Leu Thr His Gln Lys Lys Lys
65 70 75 80

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 Glu Ser Glu Asn Glu Leu Lys Glu Met Ile Glu Thr Leu Ala Arg Lys
 100 105 110
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 115 120 125
 Asn Leu Gln Glu Thr Leu Lys Arg Val Ala Asn Cys Ser Ala Pro Cys
 130 135 140
 Pro Gln Asp Trp Ile Trp His Gly Glu Asn Cys Tyr Leu Phe Ser Ser
 145 150 155 160
 Gly Ser Phe Asn Trp Glu Lys Ser Gln Glu Lys Cys Leu Ser Leu Asp
 165 170 175
 Ala Lys Leu Leu Lys Ile Asn Ser Thr Ala Asp Leu Asp Phe Ile Gln
 180 185 190
 Gln Ala Ile Ser Tyr Ser Ser Phe Pro Phe Trp Met Gly Leu Ser Arg
 195 200 205
 Arg Asn Pro Ser Tyr Pro Trp Leu Trp Glu Asp Gly Ser Pro Leu Met
 210 215 220
 Pro His Leu Phe Arg Val Arg Gly Ala Val Ser Gln Thr Tyr Pro Ser
 225 230 235 240
 Gly Thr Cys Ala Tyr Ile Gln Arg Gly Ala Val Tyr Ala Glu Asn Cys
 245 250 255
 Ile Leu Ala Ala Phe Ser Ile Cys Gln Lys Lys Ala Asn Leu Arg Ala
 260 265 270

Gln